

10 things (maybe) you didn't know about GenomicRanges, Biostrings, and Rsamtools

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1. Inner vs outer metadata columns

```
> mcols(grl)$id <- paste0("ID", seq_along(grl))
```

```
> grl
```

GRangesList object of length 3:

\$gr1

GRanges object with 1 range and 2 metadata columns:

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom2 | 3-6 | + | 5 | 0.45 |

seqinfo: 2 sequences from an unspecified genome; no seqlengths

\$gr2

GRanges object with 2 ranges and 2 metadata columns:

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 7-9 | + | 3 | 0.3 |
| [2] | Chrom1 | 13-15 | - | 4 | 0.5 |

seqinfo: 2 sequences from an unspecified genome; no seqlengths

\$gr3

GRanges object with 2 ranges and 2 metadata columns:

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 1-3 | - | 6 | 0.4 |
| [2] | Chrom2 | 4-9 | - | 2 | 0.1 |

1. Inner vs outer metadata columns

```
> mcols(gr1) # outer mcols
DataFrame with 3 rows and 1 column
      id
  <character>
gr1      ID1
gr2      ID2
gr3      ID3

> mcols(unlist(gr1, use.names=FALSE)) # inner mcols
DataFrame with 5 rows and 2 columns
      score      GC
  <integer> <numeric>
1         5      0.45
2         3      0.30
3         4      0.50
4         6      0.40
5         2      0.10
```

2. invertStrand()

Works out-of-the-box on any object that has a strand() getter and setter ==> no need to implement specific methods.

```
> gr
```

```
GRanges object with 10 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|---|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| a | chr2 | 1-10 | - | 1 | 1.000000 |
| b | chr2 | 2-10 | + | 2 | 0.888889 |
| c | chr2 | 3-10 | + | 3 | 0.777778 |
| . | ... | ... | ... | ... | ... |
| h | chr3 | 8-10 | + | 8 | 0.222222 |
| i | chr3 | 9-10 | - | 9 | 0.111111 |
| j | chr3 | 10 | - | 10 | 0.000000 |

```
-----  
seqinfo: 3 sequences from an unspecified genome; no seqlengths
```

2. invertStrand()

```
> invertStrand(gr)
```

```
GRanges object with 10 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|---|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| a | chr2 | 1-10 | + | 1 | 1.000000 |
| b | chr2 | 2-10 | - | 2 | 0.888889 |
| c | chr2 | 3-10 | - | 3 | 0.777778 |
| . | ... | ... | ... | ... | ... |
| h | chr3 | 8-10 | - | 8 | 0.222222 |
| i | chr3 | 9-10 | + | 9 | 0.111111 |
| j | chr3 | 10 | + | 10 | 0.000000 |

```
-----
```

```
seqinfo: 3 sequences from an unspecified genome; no seqlengths
```

2. invertStrand()

```
> gr1
```

```
GRangesList object of length 3:
```

```
$gr1
```

```
GRanges object with 1 range and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom2 | 3-6 | + | 5 | 0.45 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

```
$gr2
```

```
GRanges object with 2 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 7-9 | + | 3 | 0.3 |
| [2] | Chrom1 | 13-15 | - | 4 | 0.5 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

```
$gr3
```

```
GRanges object with 2 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 1-3 | - | 6 | 0.4 |
| [2] | Chrom2 | 4-9 | - | 2 | 0.1 |

2. invertStrand()

```
> invertStrand(gr1)
```

```
GRangesList object of length 3:
```

```
$gr1
```

```
GRanges object with 1 range and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom2 | 3-6 | - | 5 | 0.45 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

```
$gr2
```

```
GRanges object with 2 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 7-9 | - | 3 | 0.3 |
| [2] | Chrom1 | 13-15 | + | 4 | 0.5 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

```
$gr3
```

```
GRanges object with 2 ranges and 2 metadata columns:
```

| | seqnames | ranges | strand | score | GC |
|-----|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| [1] | Chrom1 | 1-3 | + | 6 | 0.4 |
| [2] | Chrom2 | 4-9 | + | 2 | 0.1 |

3. extractList()

Extract groups of elements from a vector-like object and return them in a list-like object.

```
> cvg <- Rle(c(0L, 2L, 5L, 1L, 0L), c(10, 6, 3, 4, 15))
> cvg
integer-Rle of length 38 with 5 runs
  Lengths: 10  6  3  4 15
  Values  :  0  2  5  1  0
> i <- IRanges(c(16, 19, 9), width=5, names=letters[1:3])
> i
IRanges object with 3 ranges and 0 metadata columns:
      start      end      width
  <integer> <integer> <integer>
a         16         20         5
b         19         23         5
c          9         13         5
```


3. `extractList()`

```
> extractList(cvg, i)
RleList of length 3
$a
integer-Rle of length 5 with 3 runs
  Lengths: 1 3 1
  Values  : 2 5 1

$b
integer-Rle of length 5 with 2 runs
  Lengths: 1 4
  Values  : 5 1

$c
integer-Rle of length 5 with 2 runs
  Lengths: 2 3
  Values  : 0 2
```

3. `extractList()`

`i` can be an `IntegerList` object:

```
> i <- IntegerList(c(25:20), NULL, seq(from=2, to=length(cvg), by=2))  
> i
```

```
IntegerList of length 3
```

```
[[1]] 25 24 23 22 21 20
```

```
[[2]] integer(0)
```

```
[[3]] 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38
```

```
> extractList(cvg, i)
```

```
RleList of length 3
```

```
[[1]]
```

```
integer-Rle of length 6 with 2 runs
```

```
  Lengths: 2 4
```

```
  Values : 0 1
```

```
[[2]]
```

```
integer-Rle of length 0 with 0 runs
```

```
  Lengths:
```

```
  Values :
```

```
[[3]]
```

```
integer-Rle of length 19 with 5 runs
```

```
  Lengths: 5 3 1 2 8
```

```
  Values : 0 2 5 1 0
```

4. 'with.revmap' arg for reduce() and (now) disjoin()

```
> ir
```

IRanges object with 6 ranges and 2 metadata columns:

| | start | end | width | | id | score |
|-----|-----------|-----------|-----------|--|-------------|-----------|
| | <integer> | <integer> | <integer> | | <character> | <integer> |
| [1] | 11 | 13 | 3 | | a | 3 |
| [2] | 12 | 14 | 3 | | b | 2 |
| [3] | 13 | 15 | 3 | | c | 1 |
| [4] | 2 | 4 | 3 | | d | 0 |
| [5] | 7 | 9 | 3 | | e | -1 |
| [6] | 6 | 8 | 3 | | f | -2 |

```
> ir2 <- reduce(ir, with.revmap=TRUE)
```

```
> ir2
```

IRanges object with 3 ranges and 1 metadata column:

| | start | end | width | | revmap |
|-----|-----------|-----------|-----------|--|---------------|
| | <integer> | <integer> | <integer> | | <IntegerList> |
| [1] | 2 | 4 | 3 | | 4 |
| [2] | 6 | 9 | 4 | | 6,5 |
| [3] | 11 | 15 | 5 | | 1,2,3 |

4. 'with.revmap' arg for reduce() and disjoint()

```
> revmap <- mcols(ir2)$revmap
> extractList(mcols(ir)$id, revmap)
CharacterList of length 3
[[1]] d
[[2]] f e
[[3]] a b c
> extractList(mcols(ir)$score, revmap)
IntegerList of length 3
[[1]] 0
[[2]] -2 -1
[[3]] 3 2 1
> mcols(ir2) <- DataFrame(id=extractList(mcols(ir)$id, revmap),
+                           score=extractList(mcols(ir)$score, revmap))
> ir2
```

IRanges object with 3 ranges and 2 metadata columns:

| | start | end | width | | id | score |
|-----|-----------|-----------|-----------|--|-----------------|---------------|
| | <integer> | <integer> | <integer> | | <CharacterList> | <IntegerList> |
| [1] | 2 | 4 | 3 | | d | 0 |
| [2] | 6 | 9 | 4 | | f,e | -2,-1 |
| [3] | 11 | 15 | 5 | | a,b,c | 3,2,1 |

5. Zero-width ranges

`findOverlaps/countOverlaps` support zero-width ranges.

```
> sliding_query <- IRanges(1:6, width=0)
> sliding_query
```

IRanges object with 6 ranges and 0 metadata columns:

| | start | end | width |
|-----|-----------|-----------|-----------|
| | <integer> | <integer> | <integer> |
| [1] | 1 | 0 | 0 |
| [2] | 2 | 1 | 0 |
| [3] | 3 | 2 | 0 |
| [4] | 4 | 3 | 0 |
| [5] | 5 | 4 | 0 |
| [6] | 6 | 5 | 0 |

```
> countOverlaps(sliding_query, IRanges(3, 4))
```

```
[1] 0 0 0 1 0 0
```

But you have to specify `minoverlap=0` for this to work (default is 1).

```
> countOverlaps(sliding_query, IRanges(3, 4), minoverlap=0)
```

```
[1] 0 0 0 1 0 0
```

6. Biostrings::replaceAt()

Perform multiple substitutions at arbitrary positions in a set of sequences.

```
> library(Biostrings)
> library(hgu95av2probe)
> probes <- DNASTringSet(hgu95av2probe)
> probes
```

DNASTringSet object of length 201800:

| | width | seq |
|----------|-------|----------------------------|
| [1] | 25 | TGGCTCCTGCTGAGGTCCCCTTTCC |
| [2] | 25 | GGCTGTGAATTCCTGTACATATTTC |
| [3] | 25 | GCTTCAATTCCATTATGTTTTAATG |
| ... | ... | ... |
| [201798] | 25 | TTCTGTCAAAGCATCATCTCAACAA |
| [201799] | 25 | CAAAGCATCATCTCAACAAGCCCTC |
| [201800] | 25 | GTGCTCCTTGTC AACAGCGCACCCA |

6. Biostrings::replaceAt()

Replace 3rd and 4th nucleotides by pattern -++-.

```
> replaceAt(probes, at=IRanges(3, 4), value="-++-")
```

DNASTringSet object of length 201800:

```
      width seq
[1]      27 TG-++-TCCTGCTGAGGTCCCCTTTCC
[2]      27 GG-++-GTGAATTCCTGTACATATTTC
[3]      27 GC-++-CAATTCATTATGTTTTAATG
...      ...
[201798] 27 TT-++-GTCAAAGCATCATCTCAACAA
[201799] 27 CA-++-GCATCATCTCAACAAGCCCTC
[201800] 27 GT-++-TCCTTGTCAACAGCGCACCCA
```

6. Biostrings::replaceAt()

If supplied pattern is empty, then performs deletions.

```
> replaceAt(probes, at=IRanges(3, 4), value="")
```

DNASTringSet object of length 201800:

| | width | seq |
|----------|-------|-------------------------|
| [1] | 23 | TGTCCTGCTGAGGTCCCCTTTCC |
| [2] | 23 | GGGTGAATTCCTGTACATATTTC |
| [3] | 23 | GCCAATTCCATTATGTTTAAATG |
| ... | ... | ... |
| [201798] | 23 | TTGTCAAAGCATCATCTCAACAA |
| [201799] | 23 | CAGCATCATCTCAACAAGCCCTC |
| [201800] | 23 | GTCCTTGTCAACAGCGCACCCA |

6. Biostrings::replaceAt()

If `at` is a zero-width range, then performs insertions.

```
> replaceAt(probes, at=IRanges(4, 3), value="--+-")
```

DNASTringSet object of length 201800:

```
      width seq
[1]      29 TGG--+-CTCCTGCTGAGGTCCCCTTTCC
[2]      29 GGC--+-TGTGAATTCCTGTACATATTTC
[3]      29 GCT--+-TCAATTCATTATGTTTTAATG
...      ...
[201798] 29 TTC--+-TGTCAAAGCATCATCTCAACAA
[201799] 29 CAA--+-AGCATCATCTCAACAAGCCCTC
[201800] 29 GTG--+-CTCCTTGTC AACAGCGCACCCA
```

6. Biostrings::replaceAt()

Use it in combination with `vmatchPattern` to replace all the occurrences of a given pattern with another pattern:

```
> midx <- vmatchPattern("VCGTT", probes, fixed=FALSE)
> replaceAt(probes, at=midx, value="-++-")
```

DNASTringSet object of length 201800:

| | width | seq |
|----------|-------|----------------------------|
| [1] | 25 | TGGCTCCTGCTGAGGTCCCCTTTCC |
| [2] | 25 | GGCTGTGAATTCCTGTACATATTTC |
| [3] | 25 | GCTTCAATTCCATTATGTTTTAATG |
| ... | ... | ... |
| [201798] | 25 | TTCTGTCAAAGCATCATCTCAACAA |
| [201799] | 25 | CAAAGCATCATCTCAACAAGCCCTC |
| [201800] | 25 | GTGCTCCTTGTC AACAGCGCACCCA |

7. GRanges as a subscript

```
> cvg <- RleList(chr1=101:120, chr2=2:-8, chr3=31:40)
> gr
```

GRanges object with 10 ranges and 2 metadata columns:

| | seqnames | ranges | strand | score | GC |
|---|----------|-----------|--------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <integer> | <numeric> |
| a | chr2 | 1-10 | - | 1 | 1.000000 |
| b | chr2 | 2-10 | + | 2 | 0.888889 |
| c | chr2 | 3-10 | + | 3 | 0.777778 |
| . | ... | ... | ... | ... | ... |
| h | chr3 | 8-10 | + | 8 | 0.222222 |
| i | chr3 | 9-10 | - | 9 | 0.111111 |
| j | chr3 | 10 | - | 10 | 0.000000 |

seqinfo: 3 sequences from an unspecified genome; no seqlengths

7. GRanges as a subscript

```
> cvg[gr]
RleList of length 10
$chr2
integer-Rle of length 10 with 10 runs
  Lengths:  1  1  1  1  1  1  1  1  1  1
  Values :  2  1  0 -1 -2 -3 -4 -5 -6 -7

$chr2
integer-Rle of length 9 with 9 runs
  Lengths:  1  1  1  1  1  1  1  1  1
  Values :  1  0 -1 -2 -3 -4 -5 -6 -7

$chr2
integer-Rle of length 8 with 8 runs
  Lengths:  1  1  1  1  1  1  1  1
  Values :  0 -1 -2 -3 -4 -5 -6 -7

$chr2
integer-Rle of length 7 with 7 runs
  Lengths:  1  1  1  1  1  1  1
  Values : -1 -2 -3 -4 -5 -6 -7

$chr1
integer-Rle of length 6 with 6 runs
  Lengths:  1  1  1  1  1  1
  Values : 105 106 107 108 109 110

...
<5 more elements>
```

8. BSgenomeViews objects

```
> library(BSgenome.Mmusculus.UCSC.mm10)
> genome <- BSgenome.Mmusculus.UCSC.mm10
> library(TxDb.Mmusculus.UCSC.mm10.knownGene)
> txdb <- TxDb.Mmusculus.UCSC.mm10.knownGene
> ex <- exons(txdb, columns=c("exon_id", "tx_name", "gene_id"))
> v <- Views(genome, ex)
```

8. BSgenomeViews objects

```
> v
```

```
BSgenomeViews object with 447558 views and 3 metadata columns:
```

| | seqnames | ranges | strand | dna |
|----------|----------------|----------------------|-----------------|---------------------------|
| | <Rle> | <IRanges> | <Rle> | <DNAStrngSet> |
| [1] | chr1 | 3073253-3074322 | + | [AAGGAAAGAG...TAGAGAAATG] |
| [2] | chr1 | 3102016-3102125 | + | [GTGCTTGCTT...ACAAAAATAT] |
| [3] | chr1 | 3252757-3253236 | + | [TTCTTCTGTG...TACCTTCAAT] |
| ... | ... | ... | ... | ... |
| [447556] | chrUn_JH584304 | 58564-58835 | - | [CTGTGTCCT...CAGAGAAATG] |
| [447557] | chrUn_JH584304 | 58564-59690 | - | [CTCTCTGCTG...CAGAGAAATG] |
| [447558] | chrUn_JH584304 | 59592-59667 | - | [AGCTGTCCCG...GCCTTCTCAG] |
| | exon_id | tx_name | gene_id | |
| | <integer> | <CharacterList> | <CharacterList> | |
| [1] | 1 | ENSMUST00000193812.1 | | |
| [2] | 2 | ENSMUST00000082908.1 | | |
| [3] | 3 | ENSMUST00000192857.1 | | |
| ... | ... | ... | ... | ... |
| [447556] | 447556 | ENSMUST00000179505.7 | 66776 | |
| [447557] | 447557 | ENSMUST00000178343.1 | 66776 | |
| [447558] | 447558 | ENSMUST00000179505.7 | 66776 | |

```
-----  
seqinfo: 239 sequences (1 circular) from mm10 genome
```

8. BSgenomeViews objects

```
> af <- alphabetFrequency(v, baseOnly=TRUE)
```

```
> head(af)
```

| | A | C | G | T | other |
|------|-----|-----|-----|-----|-------|
| [1,] | 376 | 160 | 206 | 328 | 0 |
| [2,] | 45 | 20 | 20 | 25 | 0 |
| [3,] | 138 | 105 | 86 | 151 | 0 |
| [4,] | 28 | 14 | 30 | 29 | 0 |
| [5,] | 57 | 39 | 20 | 33 | 0 |
| [6,] | 208 | 258 | 204 | 256 | 0 |

9. Pile-up statistics on a BAM file with Rsamtools::pileup()

```
> library(Rsamtools)
> library(RNAseqData.HNRNPC.bam.chr14)
> fl <- RNAseqData.HNRNPC.bam.chr14_BAMFILES[1]
> sbp <- ScanBamParam(which=GRanges("chr14", IRanges(1, 53674770)))
> pp <- PileupParam(distinguish_nucleotides=FALSE,
+                  distinguish_strands=FALSE,
+                  min_mapq=13,
+                  min_base_quality=10,
+                  min_nucleotide_depth=4)
> res <- pileup(fl, scanBamParam=sbp, pileupParam=pp)
```


9. Pile-up statistics on a BAM file with Rsamtools::pileup()

```
> dim(res)
```

```
[1] 248409      4
```

```
> head(res)
```

| | seqnames | pos | count | which_label |
|---|----------|----------|-------|------------------|
| 1 | chr14 | 19681651 | 4 | chr14:1-53674770 |
| 2 | chr14 | 19681655 | 4 | chr14:1-53674770 |
| 3 | chr14 | 19681657 | 4 | chr14:1-53674770 |
| 4 | chr14 | 19681658 | 4 | chr14:1-53674770 |
| 5 | chr14 | 19681661 | 4 | chr14:1-53674770 |
| 6 | chr14 | 19681662 | 4 | chr14:1-53674770 |

10. Merging 2 GRanges objects (added this week)

```
> x
```

```
GRanges object with 2 ranges and 3 metadata columns:
```

| | seqnames | ranges | strand | score | a1 | a2 |
|-----|----------|-----------|--------|-----------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <numeric> | <integer> | <numeric> |
| [1] | chr1 | 1-1000 | * | 0.45 | 5 | 6 |
| [2] | chr2 | 2000-3000 | * | NA | 7 | 8 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

```
> y
```

```
GRanges object with 3 ranges and 3 metadata columns:
```

| | seqnames | ranges | strand | score | b1 | b2 |
|-----|----------|-----------|--------|-----------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <numeric> | <integer> | <numeric> |
| [1] | chr2 | 150-151 | * | 0.70 | 0 | 1 |
| [2] | chr1 | 1-10 | * | 0.82 | 5 | -2 |
| [3] | chr2 | 2000-3000 | * | 0.10 | 1 | 1 |

```
-----  
seqinfo: 2 sequences from an unspecified genome; no seqlengths
```

10. Merging 2 GRanges objects

```
> merge(x, y)
```

GRanges object with 1 range and 5 metadata columns:

| | seqnames | ranges | strand | score | a1 | a2 | b1 |
|-----|----------|-----------|--------|-----------|-----------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <numeric> | <integer> | <numeric> | <integer> |
| [1] | chr2 | 2000-3000 | * | 0.1 | 7 | 8 | 1 |
| | | b2 | | | | | |
| | | <numeric> | | | | | |
| [1] | | 1 | | | | | |

seqinfo: 2 sequences from an unspecified genome; no seqlengths

10. Merging 2 GRanges objects

```
> merge(x, y, all=TRUE)
```

GRanges object with 4 ranges and 5 metadata columns:

| | seqnames | ranges | strand | score | a1 | a2 | b1 |
|-----|----------|-----------|--------|-----------|-----------|-----------|-----------|
| | <Rle> | <IRanges> | <Rle> | <numeric> | <integer> | <numeric> | <integer> |
| [1] | chr1 | 1-10 | * | 0.82 | <NA> | NA | 5 |
| [2] | chr1 | 1-1000 | * | 0.45 | 5 | 6 | <NA> |
| [3] | chr2 | 150-151 | * | 0.70 | <NA> | NA | 0 |
| [4] | chr2 | 2000-3000 | * | 0.10 | 7 | 8 | 1 |

b2

<numeric>

| | |
|-----|----|
| [1] | -2 |
| [2] | NA |
| [3] | 1 |
| [4] | 1 |

seqinfo: 2 sequences from an unspecified genome; no seqlengths